

SEQUENCE LISTING

10/563896
IAP20 Rec'd PCT/PTO 09 JAN 2006

<110> JAPAN SCIENCE AND TECHNOLOGY AGENCY
TAKEDA, Junji
HORIE, Kyoji

<120> Method and sysytem for producing transgenic organisms using
methylation

<130> KJ007PCT

<150> PCT/JP03/08681

<151> 2003-07-08

<160> 76

<170> PatentIn version 3.2

<210> 1

<211> 1455

<212> DNA

<213> Tanichthys albonubes

<220>

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<222> (1)..(1455)

<223> /note="Tcl-like transposon"

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<308> L48685

<309> 1996-05-31

<313> (1)..(1455)

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gac ctc cac aag tct ggt tca tcc ttg gga gca att tcc aaa cgc ctg 96
Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

aaa gta cca cgt tca tct gta caa aca ata gta cgc aag tat aaa cac 144
Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

cat ggg acc acg cag ccg tca tac cgc tca gga agg aga cgc gtt ctg 192
His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
50 55 60

tct cct aga gat gaa cgt act ttg gtg cga aaa gtg caa atc aat ccc 240
Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

aga aca aca gca aag gac ctt gtg aag atg ctg gag gaa aca ggt aca 288
Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

aaa gta tct ata tcc aca gta aaa cga gtc cta tat cga cat aac ctg 336
Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
100 105 110

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gaa ggc tac ccg aaa cgt ttg acc caa gtt aaa caa ttt aaa ggc aat Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn 325 330 335	1008
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Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
50 55 60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
100 105 110

Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
115 120 125

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
130 135 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145 150 155 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
195 200 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225 230 235 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
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Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
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Ile Leu Arg Ser Ala Arg Glu Asp Pro His Arg Thr Ala Thr Asp Ile						
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Gln Met Ile Ile Ser Ser Pro Asn Glu Pro Val Pro Ser Lys Arg Thr						
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Val Arg Arg Arg Leu Gln Gln Ala Gly Leu His Gly Arg Lys Pro Val						
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aag aaa ccg ttc atc agt aag aaa aat cgc atg gct cga gtt gcg tgg						726
Lys Lys Pro Phe Ile Ser Lys Lys Asn Arg Met Ala Arg Val Ala Trp						
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Ala Lys Ala His Leu Arg Trp Gly Arg Gln Glu Trp Ala Lys His Ile						
	70		75		80	
tgg tct gac gaa agc aag ttc aat ttg ttc ggg agt gat gga aat tcc						822
Trp Ser Asp Glu Ser Lys Phe Asn Leu Phe Gly Ser Asp Gly Asn Ser						
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Trp Val Arg Arg Pro Val Gly Ser Arg Tyr Ser Pro Lys Tyr Gln Cys						
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cca acc gtt aag cat gga ggt ggg agc gtc atg gtg tgg ggg tgc ttc						918
Pro Thr Val Lys His Gly Gly Gly Ser Val Met Val Trp Gly Cys Phe						
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acc agc act tcc atg ggc cca cta agg aga atc caa agc att atg gat						966
Thr Ser Thr Ser Met Gly Pro Leu Arg Arg Ile Gln Ser Ile Met Asp						
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cgt ttt caa tac gaa aac atc ttt gaa act aca atg cga ccc tgg gca						1014
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ctt caa aat gtg ggc cgt ggc ttc gtg ttt cag cag gat aac gat cct						1062
Leu Gln Asn Val Gly Arg Gly Phe Val Phe Gln Gln Asp Asn Asp Pro						
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Lys His Thr Ser Leu His Val Arg Ser Trp Phe Gln Arg Arg His Val						
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cat ttg ctc gat tgg cca agt cag tct ccg gac ttg aat cca ata gag						1158
His Leu Leu Asp Trp Pro Ser Gln Ser Pro Asp Leu Asn Pro Ile Glu						
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His Leu Trp Glu Glu Leu Glu Arg Arg Leu Gly Gly Ile Arg Ala Ser						
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245                250                255                260

caa gct gtt att gat gca aac gga tac gcg aca aag tat taa            1344
Gln Ala Val Ile Asp Ala Asn Gly Tyr Ala Thr Lys Tyr
                265                270

gcataattat gttgttttta aatccaattg ctcatattcc ggtactttaa ttgtcatttc  1404
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Ser Lys Arg Thr Val Arg Arg Arg Leu Gln Gln Ala Gly Leu His Gly
35                40                45

Arg Lys Pro Val Lys Lys Pro Phe Ile Ser Lys Lys Asn Arg Met Ala
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Arg Val Ala Trp Ala Lys Ala His Leu Arg Trp Gly Arg Gln Glu Trp
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Ala Lys His Ile Trp Ser Asp Glu Ser Lys Phe Asn Leu Phe Gly Ser
85                90                95

Asp Gly Asn Ser Trp Val Arg Arg Pro Val Gly Ser Arg Tyr Ser Pro
100               105               110

Lys Tyr Gln Cys Pro Thr Val Lys His Gly Gly Gly Ser Val Met Val
115               120               125

Trp Gly Cys Phe Thr Ser Thr Ser Met Gly Pro Leu Arg Arg Ile Gln
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Ser Ile Met Asp Arg Phe Gln Tyr Glu Asn Ile Phe Glu Thr Thr Met

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Asp Asn Asp Pro Lys His Thr Ser Leu His Val Arg Ser Trp Phe Gln
      180                185                190
Arg Arg His Val His Leu Leu Asp Trp Pro Ser Gln Ser Pro Asp Leu
      195                200                205
Asn Pro Ile Glu His Leu Trp Glu Glu Leu Glu Arg Arg Leu Gly Gly
      210                215                220
Ile Arg Ala Ser Asn Ala Asp Ala Lys Phe Asn Gln Leu Glu Asn Ala
      225                230                235                240
Trp Lys Ala Ile Pro Met Ser Val Ile His Lys Leu Ile Asp Ser Met
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Tyr

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tcgtctcaaa gagaatttta ttctcttcac gacgaaaaaa aaagttttgc tctatttcca      180

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caa ttg gca aaa ctg tca agc gag agt gga cgc gac aaa tta aaa agt Gln Leu Ala Lys Leu Ser Ser Glu Ser Gly Arg Asp Lys Leu Lys Ser 120 125 130	739
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35 40 45

Ile Ser Lys Gln Leu Asn Leu Pro Lys Ser Ser Val His Gly Val Ile
50 55 60

Gln Ile Phe Lys Lys Asn Gly Asn Ile Glu Asn Asn Ile Ala Asn Arg
65 70 75 80

Gly Arg Thr Ser Ala Ile Thr Pro Arg Asp Lys Arg Gln Leu Ala Lys
85 90 95

Ile Val Lys Ala Asp Arg Arg Gln Ser Leu Arg Asn Leu Ala Ser Lys
100 105 110

Trp Ser Gln Gln Leu Ala Lys Leu Ser Ser Glu Ser Gly Arg Asp Lys
115 120 125

Leu Lys Ser Ile Gly Tyr Gly Phe Tyr Lys Ala Lys Glu Lys Pro Leu
130 135 140

Leu Thr Leu Arg Gln Lys Lys Lys Arg Leu Gln Trp Ala Arg Glu Arg
145 150 155 160

Met Ser Trp Thr Gln Arg Gln Trp Asp Thr Ile Ile Phe Ser Asp Glu
165 170 175

Ala Lys Phe Asp Val Ser Val Gly Asp Thr Arg Lys Arg Val Ile Arg
180 185 190

Lys Arg Ser Glu Thr Tyr His Lys Asp Cys Leu Lys Arg Thr Thr Lys
195 200 205

Phe Pro Ala Ser Thr Met Val Trp Gly Cys Met Ser Ala Lys Gly Leu
210 215 220

Gly Lys Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile
225 230 235 240

Asn Ile Leu Gln Asp Ser Leu Leu Pro Ser Ile Pro Lys Leu Leu Asp
245 250 255

Cys Gly Glu Phe Thr Phe Gln Gln Asp Gly Ala Ser Ser His Thr Ala
260 265 270

Lys Arg Thr Lys Asn Trp Leu Gln Tyr Asn Gln Met Glu Val Leu Asp
275 280 285

Trp Pro Ser Asn Ser Pro Asp Leu Ser Pro Ile Glu Asn Ile Trp Trp
290 295 300

Leu Met Lys Asn Gln Leu Arg Asn Glu Pro Gln Arg Asn Ile Ser Asp
 305 310 315 320

Leu Lys Ile Lys Leu Gln Glu Met Trp Asp Ser Ile Ser Gln Glu His
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Gln Ala Lys Gly Asp Val Thr Gln Phe
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 acaacaacaa aaatatgagt aatttattca aacgggtttgc ttaagagata agaaaaaagt 240
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 Met Ser Gln
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tac agc atg caa aaa aat ttt aga ttg ctg cag atc agt aga agt tta 403
 Tyr Ser Met Gln Lys Asn Phe Arg Leu Leu Gln Ile Ser Arg Ser Leu
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gca acg atg gtt cgt ggt aaa cct att tct aaa gaa atc aga gta ttg 451
 Ala Thr Met Val Arg Gly Lys Pro Ile Ser Lys Glu Ile Arg Val Leu
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att agg gat tat ttt aaa tct gga aag aca ctt acg gag ata agc aag 499
 Ile Arg Asp Tyr Phe Lys Ser Gly Lys Thr Leu Thr Glu Ile Ser Lys
 40 45 50

caa tta aat ttg cct aag tcg tct gtg cat ggg gtg ata caa att ttc Gln Leu Asn Leu Pro Lys Ser Ser Val His Gly Val Ile Gln Ile Phe 55 60 65	547
aaa aaa aat ggg aat att gaa aat aac att gcg aat aga ggc cga aca Lys Lys Asn Gly Asn Ile Glu Asn Asn Ile Ala Asn Arg Gly Arg Thr 70 75 80	595
tca gca ata aca ccc cgc gac aaa aga caa ctg gcc aaa att gtt aag Ser Ala Ile Thr Pro Arg Asp Lys Arg Gln Leu Ala Lys Ile Val Lys 85 90 95	643
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caa ttg gca aaa ctg tca agc gag agt gga cgc gac aaa tta aaa agt Gln Leu Ala Lys Leu Ser Ser Glu Ser Gly Arg Asp Lys Leu Lys Ser 120 125 130	739
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gcg agc act atg gta tgg gga tgt atg tct gcc aaa gga tta gga aaa Ala Ser Thr Met Val Trp Gly Cys Met Ser Ala Lys Gly Leu Gly Lys 215 220 225	1084
ctt cat ttc att gaa ggg aca gtt aat gct gaa aaa tat att aat att Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile Asn Ile 230 235 240	1132
tta caa gat agt ttg ttg cca tca ata cca aaa cta tca gat tgc ggt Leu Gln Asp Ser Leu Leu Pro Ser Ile Pro Lys Leu Ser Asp Cys Gly 245 250 255	1180
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acc aaa aat tgg ctg caa tat aat caa atg gag gtt tta gat tgg cca Thr Lys Asn Trp Leu Gln Tyr Asn Gln Met Glu Val Leu Asp Trp Pro 275 280 285 290	1276
tca aat agt cca gat cta agc cca att gaa aat att tgg tgg cta atg	1324

Ser Asn Ser Pro Asp Leu Ser Pro Ile Glu Asn Ile Trp Trp Leu Met
 295 300 305
 aaa aac cag ctt cga aat gag cca caa agg aat att tct gac ttg aaa 1372
 Lys Asn Gln Leu Arg Asn Glu Pro Gln Arg Asn Ile Ser Asp Leu Lys
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 atc aag ttg caa gag atg tgg gac tca att tct caa gag cat tgc aaa 1420
 Ile Lys Leu Gln Glu Met Trp Asp Ser Ile Ser Gln Glu His Cys Lys
 325 330 335
 aat ttg tta agc tca atg cca aaa cga gtt aaa tgc gta atg cag gcc 1468
 Asn Leu Leu Ser Ser Met Pro Lys Arg Val Lys Cys Val Met Gln Ala
 340 345 350
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 Lys Gly Asp Val Thr Gln Phe
 355 360
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 aagcaaacgcg tttgaataaa ttactcatat ttttggtggt gttggaaata gagcaaaact 1639
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 35 40 45

Ile Ser Lys Gln Leu Asn Leu Pro Lys Ser Ser Val His Gly Val Ile
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Gln Ile Phe Lys Lys Asn Gly Asn Ile Glu Asn Asn Ile Ala Asn Arg
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Gly Arg Thr Ser Ala Ile Thr Pro Arg Asp Lys Arg Gln Leu Ala Lys
 85 90 95

Ile Val Lys Ala Asp Arg Arg Gln Ser Leu Arg Asn Leu Ala Ser Lys
 100 105 110

Trp Ser Gln Gln Leu Ala Lys Leu Ser Ser Glu Ser Gly Arg Asp Lys

115

120

125

Leu Lys Ser Ile Gly Tyr Gly Phe Tyr Lys Ala Lys Glu Lys Pro Leu
 130 135 140

Leu Thr Leu Arg Gln Lys Lys Lys Arg Leu Gln Trp Ala Arg Glu Arg
 145 150 155 160

Met Ser Trp Thr Gln Arg Gln Trp Asp Thr Ile Ile Phe Ser Asp Glu
 165 170 175

Ala Lys Phe Asp Val Ser Val Gly Asp Thr Arg Lys Arg Val Ile Arg
 180 185 190

Lys Arg Ser Glu Thr Tyr His Lys Asp Cys Leu Lys Arg Thr Thr Lys
 195 200 205

Phe Pro Ala Ser Thr Met Val Trp Gly Cys Met Ser Ala Lys Gly Leu
 210 215 220

Gly Lys Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile
 225 230 235 240

Asn Ile Leu Gln Asp Ser Leu Leu Pro Ser Ile Pro Lys Leu Ser Asp
 245 250 255

Cys Gly Glu Phe Thr Phe Gln Gln Asp Gly Ala Ser Ser His Thr Ala
 260 265 270

Lys Arg Thr Lys Asn Trp Leu Gln Tyr Asn Gln Met Glu Val Leu Asp
 275 280 285

Trp Pro Ser Asn Ser Pro Asp Leu Ser Pro Ile Glu Asn Ile Trp Trp
 290 295 300

Leu Met Lys Asn Gln Leu Arg Asn Glu Pro Gln Arg Asn Ile Ser Asp
 305 310 315 320

Leu Lys Ile Lys Leu Gln Glu Met Trp Asp Ser Ile Ser Gln Glu His
 325 330 335

Cys Lys Asn Leu Leu Ser Ser Met Pro Lys Arg Val Lys Cys Val Met
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Gln Ala Lys Gly Asp Val Thr Gln Phe
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<213> Haematobia irritans

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Met Glu Lys Glu Phe Arg Val Leu
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ata aaa tac tgt ttt ctg aag gga aaa aat gcg gtg gaa gca aaa agt	400
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Trp Leu Asp Asn Glu Phe Pro Asp Ser Ala Pro Arg Lys Ser Ile Ile

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att gat tgg tat gca aaa ttc aag cga ggt gaa atg agc acg gag gac	496
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Ile Asp Trp Tyr Ala Lys Phe Lys Arg Gly Glu Met Ser Thr Glu Asp

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ggt gaa cgc agt gga cgc ccg aaa gag gtg gtt acc gac gaa aac atc	544
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Gly Glu Arg Ser Gly Arg Pro Lys Glu Val Val Thr Asp Glu Asn Ile

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aaa aaa atc cac aaa atg att ttg aat gac cgt aaa atg aag ttg atc	592
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Lys Lys Ile His Lys Met Ile Leu Asn Asp Arg Lys Met Lys Leu Ile

75

80

85

gag ata aca aag gcc tta aac ata tca aag gaa cgt gtt ggt cat atc	640
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Glu Ile Thr Lys Ala Leu Asn Ile Ser Lys Glu Arg Val Gly His Ile

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95

100

att cat caa tat ttg gat atg ccg aag ctc tgt gca aaa tgg gtg ccg	688
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Ile His Gln Tyr Leu Asp Met Arg Lys Leu Cys Ala Lys Trp Val Pro

105

110

115

120

cgc gaa ctc aca ttt gac caa aaa caa caa cgt gtt gat gat tct gag	736
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Arg Glu Leu Thr Phe Asp Gln Lys Gln Gln Arg Val Asp Asp Ser Glu

125

130

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cgg tgt ttg cag ctg tta act cgt aat aca ccc gag ttt ttc cgt cga	784
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Arg Cys Leu Gln Leu Leu Thr Arg Asn Thr Pro Glu Phe Phe Arg Arg

140

145

150

tat gta aca atg gat gaa aca tgg ctc cat cac tac act cct gag ttc	832
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Tyr Val Thr Met Asp Glu Thr Trp Leu His His Tyr Thr Pro Glu Phe

155

160

165

gat caa cag tcg gct gag tgg aca gcg acc ggt gaa ccg tct ccg aag	880
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Asp Gln Gln Ser Ala Glu Trp Thr Ala Thr Gly Glu Pro Ser Pro Lys

170

175

180

cgt gga aag act caa aag tcc gct ggc aaa gta atg gcc tct gtt ttt 928
 Arg Gly Lys Thr Gln Lys Ser Ala Gly Lys Val Met Ala Ser Val Phe
 185 190 195 200

tgg aat gcg cat gga ata att ttt atc gat tat ctt gag aag gaa aaa 976
 Trp Asn Ala His Gly Ile Ile Phe Ile Asp Tyr Leu Glu Lys Glu Lys
 205 210 215

acc atc aac agt gac tat tat atg gcg tta ttg gag cgt ttg aag gtc 1024
 Thr Ile Asn Ser Asp Tyr Tyr Met Ala Leu Leu Glu Arg Leu Lys Val
 220 225 230

gaa atc gcg gca aaa tgg ccc cat atg aag aag aaa aaa gtg ttg ttc 1072
 Glu Ile Ala Ala Lys Trp Pro His Met Lys Lys Lys Lys Val Leu Phe
 235 240 245

gac caa gac aat gca ccg tgc cac aag tca gta aga acg atg gca aaa 1120
 Asp Gln Asp Asn Ala Pro Cys His Lys Ser Val Arg Thr Met Ala Lys
 250 255 260

att cat gaa ttg ggc ttc gaa ttg ctt ccc cac cca cta tat tct cca 1168
 Ile His Glu Leu Gly Phe Glu Leu Leu Pro His Pro Leu Tyr Ser Pro
 265 270 275 280

gat ctg gcc ccc agc gaa ttt ttc ttg ttc tca gac ctc aaa agg ctc 1216
 Asp Leu Ala Pro Ser Glu Phe Phe Leu Phe Ser Asp Leu Lys Arg Leu
 285 290 295

gca ggg aaa aaa ttt ggc tgc aat gaa gag gta atc gcc gaa act aag 1264
 Ala Gly Lys Lys Phe Gly Cys Asn Glu Glu Val Ile Ala Glu Thr Lys
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gcc tat ttt gag gca aaa ccg aaa gag tac tac caa aat ggt atc aaa 1312
 Ala Tyr Phe Glu Ala Lys Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys
 315 320 325

aaa ttg gaa ggt cgt tat aat cgt ggt atc gct ctt gaa ggg gac tat 1360
 Lys Leu Glu Gly Arg Tyr Asn Arg Gly Ile Ala Leu Glu Gly Asp Tyr
 330 335 340

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 Val Glu
 345

gacttatcac ccaacctgtt aaaaactgtt actttttgtt aaagtaagtc agaataaaaac 1476

aaatatattga atttttgagg gtgtacgtaa acttctttga ttcactgtat atatttttaa 1536

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<212> PRT

<213> Haematobia irritans

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35 40 45

Arg Gly Glu Met Ser Thr Glu Asp Gly Glu Arg Ser Gly Arg Pro Lys
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Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile Leu
65 70 75 80

Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Thr Lys Ala Leu Asn Ile
85 90 95

Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met Arg
100 105 110

Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Phe Asp Gln Lys
115 120 125

Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr Arg
130 135 140

Asn Thr Pro Glu Phe Phe Arg Arg Tyr Val Thr Met Asp Glu Thr Trp
145 150 155 160

Leu His His Tyr Thr Pro Glu Phe Asp Gln Gln Ser Ala Glu Trp Thr
165 170 175

Ala Thr Gly Glu Pro Ser Pro Lys Arg Gly Lys Thr Gln Lys Ser Ala
180 185 190

Gly Lys Val Met Ala Ser Val Phe Trp Asn Ala His Gly Ile Ile Phe
195 200 205

Ile Asp Tyr Leu Glu Lys Glu Lys Thr Ile Asn Ser Asp Tyr Tyr Met
210 215 220

Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Trp Pro His
225 230 235 240

Met Lys Lys Lys Lys Val Leu Phe Asp Gln Asp Asn Ala Pro Cys His
245 250 255

Lys Ser Val Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu Leu
260 265 270

Leu Pro His Pro Leu Tyr Ser Pro Asp Leu Ala Pro Ser Glu Phe Phe
275 280 285

Leu Phe Ser Asp Leu Lys Arg Leu Ala Gly Lys Lys Phe Gly Cys Asn
290 295 300

Glu Glu Val Ile Ala Glu Thr Lys Ala Tyr Phe Glu Ala Lys Pro Lys
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gcttgcttaa tatcggctct ctgtatatta gggtggctga taagtccccg gtctgacaca 180
tagatggcgt cgctagtatt aaatgcatat tatttttata tagtaccaac cttcaaata 240
ttcgtgtcaa aatttgacgt ctgtaagtca attagtttgt gagatagagc gtcttttgtg 300
aagcaacttt tgttattgtg aaaaaa atg gaa aaa aag gaa ttt cgt gtt ttg 353
Met Glu Lys Lys Glu Phe Arg Val Leu
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ata aaa tac tgt ttt ctg aag gga aaa aat aca gtg gaa gca aaa act 401
Ile Lys Tyr Cys Phe Leu Lys Gly Lys Asn Thr Val Glu Ala Lys Thr
10 15 20 25
tgg ctt gat aat gag ttt ccg gac tct gcc cca ggg aaa tca aca ata 449
Trp Leu Asp Asn Glu Phe Pro Asp Ser Ala Pro Gly Lys Ser Thr Ile
30 35 40
att gat tgg tat gca aaa ttc aag cgt ggt gaa atg agc acg gag gac 497
Ile Asp Trp Tyr Ala Lys Phe Lys Arg Gly Glu Met Ser Thr Glu Asp
45 50 55
ggt gaa cgc agt gga cgc ccg aaa gag gtg gtt acc gac gaa aac atc 545
Gly Glu Arg Ser Gly Arg Pro Lys Glu Val Val Thr Asp Glu Asn Ile
60 65 70

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Lys	Lys	Ile	His	Lys	Met	Ile	Leu	Asn	Asp	Arg	Lys	Met	Lys	Leu	Ile	
75						80					85					
gag	ata	gca	gag	gcc	tta	aag	ata	tca	aag	gaa	cgt	gtt	ggt	cat	atc	641
Glu	Ile	Ala	Glu	Ala	Leu	Lys	Ile	Ser	Lys	Glu	Arg	Val	Gly	His	Ile	
90					95					100					105	
att	cat	caa	tat	ttg	gat	atg	cgg	aag	ctc	tgt	gca	aaa	tgg	gtg	ccg	689
Ile	His	Gln	Tyr	Leu	Asp	Met	Arg	Lys	Leu	Cys	Ala	Lys	Trp	Val	Pro	
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cgc	gag	ctc	aca	ttt	gac	caa	aaa	caa	caa	cgt	gtt	gat	gat	tct	gag	737
Arg	Glu	Leu	Thr	Phe	Asp	Gln	Lys	Gln	Gln	Arg	Val	Asp	Asp	Ser	Glu	
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Arg	Cys	Leu	Gln	Leu	Leu	Thr	Arg	Asn	Thr	Pro	Glu	Phe	Leu	Arg	Arg	
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Tyr	Val	Thr	Met	Asp	Glu	Thr	Trp	Leu	His	His	Tyr	Thr	Pro	Glu	Ser	
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Lys	Arg	Gln	Ser	Ala	Glu	Trp	Thr	Ala	Thr	Gly	Glu	Pro	Ser	Pro	Lys	
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cgt	gga	aag	act	caa	aag	tcc	gct	ggc	aaa	gta	atg	gcc	tct	gtt	ttt	929
Arg	Gly	Lys	Thr	Gln	Lys	Ser	Ala	Gly	Lys	Val	Met	Ala	Ser	Val	Phe	
				190					195					200		
ttc	gat	gcg	cat	gga	ata	att	ttt	atc	gat	tat	ctt	gag	aag	gga	aaa	977
Phe	Asp	Ala	His	Gly	Ile	Ile	Phe	Ile	Asp	Tyr	Leu	Glu	Lys	Gly	Lys	
			205					210					215			
acc	atc	aac	agt	gac	tat	tat	atg	gcg	tta	ttg	gag	cgt	ttg	aag	gtc	1025
Thr	Ile	Asn	Ser	Asp	Tyr	Tyr	Met	Ala	Leu	Leu	Glu	Arg	Leu	Lys	Val	
		220					225					230				
gaa	atc	gcg	gca	aaa	cgg	ccc	cat	atg	aag	aag	aaa	aaa	gtg	ttg	ttc	1073
Glu	Ile	Ala	Ala	Lys	Arg	Pro	His	Met	Lys	Lys	Lys	Lys	Val	Leu	Phe	
	235					240					245					
cac	caa	gac	aac	gca	ccg	tgc	cac	aag	tca	ttg	aga	acg	atg	gca	aaa	1121
His	Gln	Asp	Asn	Ala	Pro	Cys	His	Lys	Ser	Leu	Arg	Thr	Met	Ala	Lys	
250						255				260					265	
att	cat	gaa	ttg	ggc	ttc	gaa	ttg	ctt	ccc	cac	cca	ccg	tat	tct	cca	1169
Ile	His	Glu	Leu	Gly	Phe	Glu	Leu	Leu	Pro	His	Pro	Pro	Tyr	Ser	Pro	
				270					275					280		
gat	ctg	gcc	ccc	agc	gac	ttt	ttc	ttg	ttc	tca	gac	ctc	aaa	agg	atg	1217
Asp	Leu	Ala	Pro	Ser	Asp	Phe	Phe	Leu	Phe	Ser	Asp	Leu	Lys	Arg	Met	
			285					290					295			
ctc	gca	ggg	aaa	aaa	ttt	ggc	tgc	aat	gaa	gag	gtg	atc	gcc	gaa	act	1265
Leu	Ala	Gly	Lys	Lys	Phe	Gly	Cys	Asn	Glu	Glu	Val	Ile	Ala	Glu	Thr	
		300					305					310				
gag	gcc	tat	ttt	gag	gca	aaa	ccg	aag	gag	tac	tac	caa	aat	ggt	atc	1313
Glu	Ala	Tyr	Phe	Glu	Ala	Lys	Pro	Lys	Glu	Tyr	Tyr	Gln	Asn	Gly	Ile	
	315					320					325					
aaa	aaa	ttg	gaa	ggt	cgt	tat	aat	cgt	tgt	atc	gct	ctt	gaa	ggg	aac	1361

Lys Lys Leu Glu Gly Arg Tyr Asn Arg Cys Ile Ala Leu Glu Gly Asn
 330 335 340 345

tat gtt gaa taa taaaaacgaa ttttcacaaa aaaatgtgtt tttctttgtt 1413
 Tyr Val Glu

agaccgggga cttatcagcc aacctgttat cttgacgaaa aaatgaatgg tcgataaata 1473

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<211> 348

<212> PRT

<213> Chrysoperla plorabunda

<400> 19

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Gly Lys Asn Thr Val Glu Ala Lys Thr Trp Leu Asp Asn Glu Phe Pro
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Asp Ser Ala Pro Gly Lys Ser Thr Ile Ile Asp Trp Tyr Ala Lys Phe
 35 40 45

Lys Arg Gly Glu Met Ser Thr Glu Asp Gly Glu Arg Ser Gly Arg Pro
 50 55 60

Lys Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile
 65 70 75 80

Leu Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Ala Glu Ala Leu Lys
 85 90 95

Ile Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met
 100 105 110

Arg Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Phe Asp Gln
 115 120 125

Lys Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr
 130 135 140

Arg Asn Thr Pro Glu Phe Leu Arg Arg Tyr Val Thr Met Asp Glu Thr
 145 150 155 160

Trp Leu His His Tyr Thr Pro Glu Ser Lys Arg Gln Ser Ala Glu Trp
 165 170 175

Thr Ala Thr Gly Glu Pro Ser Pro Lys Arg Gly Lys Thr Gln Lys Ser

180

185

190

Ala Gly Lys Val Met Ala Ser Val Phe Phe Asp Ala His Gly Ile Ile
195 200 205

Phe Ile Asp Tyr Leu Glu Lys Gly Lys Thr Ile Asn Ser Asp Tyr Tyr
210 215 220

Met Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Arg Pro
225 230 235 240

His Met Lys Lys Lys Lys Val Leu Phe His Gln Asp Asn Ala Pro Cys
245 250 255

His Lys Ser Leu Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu
260 265 270

Leu Leu Pro His Pro Pro Tyr Ser Pro Asp Leu Ala Pro Ser Asp Phe
275 280 285

Phe Leu Phe Ser Asp Leu Lys Arg Met Leu Ala Gly Lys Lys Phe Gly
290 295 300

Cys Asn Glu Glu Val Ile Ala Glu Thr Glu Ala Tyr Phe Glu Ala Lys
305 310 315 320

Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys Lys Leu Glu Gly Arg Tyr
325 330 335

Asn Arg Cys Ile Ala Leu Glu Gly Asn Tyr Val Glu
340 345

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<211> 378
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<220>
<223> IR/DR-R

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aattccatca caaagctctg acctcaatcc tatagaaagg aggaatgagc caaaattcac 60
ccaacttatt gtgggaagct tgtggaaggc tactcgaaat gtttgacca agttaaacaa 120
tttaaaggca atgctaccaa atactaattg agtgtatgtt aacttctgac ccaactgggaa 180
tgtgatgaaa gaaataaaaag ctgaaatgaa tcattctctc tactattatt ctgatatttc 240
acattcttaa aataaagtgg tgatcctaac tgaccttaag acaggaatc ttactcgga 300
ttaaatgtca ggaattgtga aaaagtgagt ttaaatgtat ttggctaagg tgtatgtaa 360
cttccgactt caactgta 378

<210> 21
 <211> 354
 <212> DNA
 <213> Artificial

<220>
 <223> IR/DR-L

<400> 21
 ccttgaaata catccacagg tacacctcca attgactcaa atgatgtcaa ttagtctatc 60
 agaagcttct aaagccatga catcattttc tggaattttc caagctgttt aaaggcacag 120
 tcaacttagt gtatgtaaac ttctgacca ctggaattgt gatacagtga attataagt 180
 aaataatctg tctgtaaaca attgttgga aaatgacttg tgtcatgcac aaagtagatg 240
 tcctaactga cttgccaaaa ctattgtttg ttaacaagaa atttgtggag tagttgaaaa 300
 acgagtttta atgactccaa ctttaagtga tgtaaacttc cgacttcaac tgta 354

<210> 22
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> 5' outer repeat

<400> 22
 gttcaagtcg gaagtttaca tacacttag 29

<210> 23
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> 5' inner repeat

<400> 23
 cagtgggtca gaagtttaca tacactaagg 30

<210> 24
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> 3' inner repeat

<400> 24
 cagtgggtca gaagttaaca tacactcaat t 31

<210> 25
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> 3' outer repeat

<400> 25
agttgaatcg gaagttttaca tacaccttag 30

<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>
<223> preferred consensus direct repeat

<400> 26
caktgrgtcr gaagttttaca tacacttaag 30

<210> 27
<211> 26
<212> DNA
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<220>
<223> inverted repeat sequence

<400> 27
gttgaagtcg gaagttttaca cttagg 26

<210> 28
<211> 31
<212> DNA
<213> Artificial

<220>
<223> inverted repeat sequence

<400> 28
ccagtgggtc aggaagttta catacactaa g 31

<210> 29
<211> 27
<212> DNA
<213> Artificial

<220>
<223> forward sequence used for PCR amplication from pCMV-SB

<400> 29
catgccatgg gaaaatcaaa agaaatc 27

<210> 30
<211> 26
<212> DNA
<213> Artificial

<220>
<223> reverse sequence used for PCR amplication from pCMV-SB

<400> 30
ccgctcgagc agtggcttct tccttg 26

<210> 31

<211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> primer EGFP-1U

<400> 31
 caccctcgtg accaccctga cctac

25

<210> 32
 <211> 25
 <212> DNA
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<220>
 <223> primer EGFP-1L

<400> 32
 cttgatgccg ttcttctgct tgctcg

25

<210> 33
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 <212> DNA
 <213> Artificial

<220>
 <223> primer HYG-1U

<400> 33
 cgggcgtata tgctcccat tggctcttgac

30

<210> 34
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<220>
 <223> primer TK-1L

<400> 34
 tgggttagat gttcgcgatt gtctcggaag

30

<210> 35
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<220>
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<400> 35
 acgacgttgt aaaacgacgg ccagt

25

<210> 36
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<220>
 <223> primer RMCE-DL1

<400> 36
gcacgcgcat gggtcacgac gagatcctc 29

<210> 37
<211> 30
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<220>
<223> RRMCE-IL-1

<400> 37
aagtgagttt aaatgtattt ggctaaggtg 30

<210> 38
<211> 30
<212> DNA
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<220>
<223> TgTP-2L

<400> 38
acacaggaaa cagctatgac catgattacg 30

<210> 39
<211> 25
<212> DNA
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<220>
<223> primer neo-U1

<400> 39
gggtggagag gctattcggc tatga 25

<210> 40
<211> 25
<212> DNA
<213> Artificial

<220>
<223> primer neo-L1

<400> 40
tggatacttt ctcggcagga gcaag 25

<210> 41
<211> 23
<212> DNA
<213> Artificial

<220>
<223> probe

<220>
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<222> (23)..(23)
<223> connected to FITC

<400> 41
cggccgctct agcgggtaccc tac

23

<210> 42
<211> 22
<212> DNA
<213> Artificial

<220>
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<220>
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<222> (1)..(1)
<223> connected to LCRed640

<400> 42
gtaggggatc gacctcgagg gg

22

<210> 43
<211> 25
<212> DNA
<213> Artificial

<220>
<223> probe

<220>
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<222> (1)..(1)
<223> connected to FITC

<400> 43
gctgtgctcg acgttgtcac tgaag

25

<210> 44
<211> 24
<212> DNA
<213> Artificial

<220>
<223> probe

<220>
<221> misc_feature
<222> (1)..(1)
<223> connected to LCRed640

<400> 44
gggaaggac tggctgctat tggg

24

<210> 45
<211> 20
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 45
gttgggtcgt ttgttcggat 20

<210> 46
<211> 20
<212> DNA
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<220>
<223> PCR primer

<400> 46
cgcgcaatta accctcacta 20

<210> 47
<211> 20
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 47
aatgaactgc aggacgaggc 20

<210> 48
<211> 20
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 48
atggatactt tctcggcagg 20

<210> 49
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer LCB2XL2

<400> 49
ttccaaaaga agtagagtgg agaaccagtg 30

<210> 50
<211> 23
<212> DNA
<213> Artificial

<220>
<223> primer PGK2

<400> 50
aggccacttg tgtagcgcca agt 23

<210> 51

<211> 30
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<220>
<223> primer LCB2XL1

<400> 51
ccaaccaa acatttaaca tattctaggt

30

<210> 52
<211> 26
<212> DNA
<213> Artificial

<220>
<223> primer PGK4

<400> 52
gctgctaaag cgcattgctcc agactg

26

<210> 53
<211> 30
<212> DNA
<213> Artificial

<220>
<223> forward primer for amplification of SB transposase gene

<400> 53
aatagaactg ttggtccata atgaccatcg

30

<210> 54
<211> 25
<212> DNA
<213> Artificial

<220>
<223> reverse primer for amplification of SB transposase gene

<400> 54
atccacataa ttttccttcc tcatg

25

<210> 55
<211> 30
<212> DNA
<213> Artificial

<220>
<223> forward primer for amplification of beta actin transposase gene

<400> 55
cagggtgtga tgggtgggaat gggtcagaag

30

<210> 56
<211> 30
<212> DNA
<213> Artificial

<220>
<223> reverse primer for amplification of beta actin transposase gene

<400> 56
tacgtacatg gctggggtgt tgaaggtctc

30

<210> 57
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer beta geo

<400> 57
tgccagtttg aggggacgac gacagtatcg

30

<210> 58
<211> 30
<212> DNA
<213> Artificial

<220>
<223> MS specific primer

<400> 58
tggagtgagc tagaatcaga aagatgacac

30

<210> 59
<211> 30
<212> DNA
<213> Artificial

<220>
<223> M2L specific primer

<400> 59
gactttcaag accttcgacg caccgttcac

30

<210> 60
<211> 30
<212> DNA
<213> Artificial

<220>
<223> M4 specific primer

<400> 60
tcttcagcca caggctccca gacatgacag

30

<210> 61
<211> 30
<212> DNA
<213> Artificial

<220>
<223> N1 specific primer

<400> 61
gatatgaaga gctgtcagtt tgtagcagtc

30

<210> 62

<211> 34
<212> DNA
<213> Artificial

<220>
<223> Unmet-U

<400> 62
tacagttgaa gtcggaagtt tacatacact taag

34

<210> 63
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Unmet-L

<400> 63
cttaagtgtgta tgtaaacttc cgacttcaac tgta

34

<210> 64
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Met-U

<220>
<221> misc_feature
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<223> N is 5-methyl cytosine

<400> 64
tacagttgaa gtnggaagtt tacatacact taag

34

<210> 65
<211> 34
<212> DNA
<213> Artificial

<220>
<223> Met-L

<220>
<221> misc_feature
<222> (21)..(21)
<223> N is 5-methyl cytosine

<400> 65
cttaagtgtgta tgtaaacttc ngacttcaac tgta

34

<210> 66
<211> 25
<212> DNA
<213> Artificial

<220>
<223> forward primer for amylase 2.1 gene

<400> 66
ccttgtagcg gttggtggag gtcac

25

<210> 67
<211> 25
<212> DNA
<213> Artificial

<220>
<223> reverse primer for amylase 2.1 gene

<400> 67
cgccactcga acaggtggac aatag

25

<210> 68
<211> 24
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 68
tgcgaggata agaacagaca ctac

24

<210> 69
<211> 24
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 69
acagactcag aagcaaactg aaga

24

<210> 70
<211> 24
<212> DNA
<213> Artificial

<220>
<223> forward primer sequence for IR/DR-L

<400> 70
gcacgggtgt tgggtcgttt gttc

24

<210> 71
<211> 27
<212> DNA
<213> Artificial

<220>
<223> reverse primer sequence for IR/DR-L

<400> 71
cttctaaagc catgacatca ttttctg

27

<210> 72

<211> 28
<212> DNA
<213> Artificial

<220>
<223> forward primer sequence for IR/DR-R

<400> 72
gaaggctact cgaaatgttt gacccaag 28

<210> 73
<211> 24
<212> DNA
<213> Artificial

<220>
<223> EGFP-1U primer

<400> 73
cacgctggtg accagcctga ccta 24

<210> 74
<211> 24
<212> DNA
<213> Artificial

<220>
<223> EGFP-1L primer

<400> 74
cttgatgccg ttctctgctt gtcg 24

<210> 75
<211> 24
<212> DNA
<213> Artificial

<220>
<223> SB-2U primer

<400> 75
tcctagagat gaacgtactt tggt 24

<210> 76
<211> 25
<212> DNA
<213> Artificial

<220>
<223> SB-1L primer

<400> 76
atccagataa ttttccttgcc tcatg 25